



SEQUENCE LISTING

GENERAL INFORMATION:

(i) APPLICANT: Eaton, Dan L.
DeSauvage, Frederic J.

(ii) TITLE OF INVENTION: MPL LIGAND

10 (iii) NUMBER OF SEQUENCES: 32

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

25 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 13-APR-1995
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/223263
(B) FILING DATE: 04-APR-1994

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/196689
(B) FILING DATE: 15-FEB-1994

40 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/185607
(B) FILING DATE: 21-JAN-1994

45 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/176553
(B) FILING DATE: 03-JAN-1994

(viii) ATTORNEY/AGENT INFORMATION:

50 (A) NAME: Winter, Daryl B.
(B) REGISTRATION NUMBER: 32,637
(C) REFERENCE/DOCKET NUMBER: 871P3D1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1249
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids
(B) TYPE: amino acid
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
1 5 10 15
Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
20 20 25 30
Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
35 40 45
Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
50 55 60
25 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
65 70 75
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
80 85 90
30 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
95 100 105
35 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
110 115 120
Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
125 130 135
40 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
140 145 150
Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
45 155 160 165
Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
170 175 180
50 Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
185 190 195

Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
 200 205 210
 5 Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
 215 220 225
 Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
 230 235 240
 10 Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
 245 250 255
 Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
 260 265 270
 15 Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
 275 280 285
 Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
 290 295 300
 Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
 305 310 315
 25 Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
 320 325 330
 Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
 335 340 345
 30 Ser Gln Asn Leu Ser Gln Glu Gly
 350 353

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
 CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
 CCCACCCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150

CCCAGCAAGG ATTCAGGGGA GAGGCCCAA ACAGGGAGCC ACGCCAGCCA 200
 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
 AGACTGAGCC AGTGCCGAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
 ATGGCAGCAC GGGGACAACT GGGACCACT TGCCTCTCAT CCCTCCTGGG 550
 GCAGCTTTCT GGACAGGTCC GTCTCCTCT TGGGGCCCTG CAGAGCCTCC 600
 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
 CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGGGG GCCCCACCCA 750
 CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
 AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC 1000
 TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050

CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100
 5 CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150
 CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200
 10 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
 TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
 15 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350
 AACTGGACAA GATTTCTTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
 GGGATACACA GGA CTGAAAA GGAATCATT TTCTACTGTA CATTATAAAC 1450
 25 CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
 GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550
 30 TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700
 40 CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750
 AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAA 1795
 45

(2) INFORMATION FOR SEQ ID NO:3:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
1 5 10 15
Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
20 25 30
10 Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
35 40 42

(2) INFORMATION FOR SEQ ID NO:4:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100
30 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CTTGCTTGTG ACCTCCGAGT 150
B¹
ent
35 CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA 200
GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA 250
40 CTCCCAGGAA GACACCATCA CTTCTCTAA CTCCTTGACC CAATGACTAT 300
TCTTCCATA TTGTCCCCAC CTAAGTATCA CACTCTCTGA CAAGAAATTAT 350
45 TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA 390

50 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA 50
GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA 100
CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA 150
GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT 200
CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT 250
GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA 300
AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA 350
AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT 390

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15
Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp
35 40 45

	Phe	Ser	Leu	Gly	Glu	Trp	Lys	Thr	Gln	Met	Glu	Glu	Thr	Lys	Ala
					50					55					60
5	Gln	Asp	Ile	Leu	Gly	Ala	Val	Thr	Leu	Leu	Leu	Glu	Gly	Val	Met
					65					70					75
	Ala	Ala	Arg	Gly	Gln	Leu	Gly	Pro	Thr	Cys	Leu	Ser	Ser	Leu	Leu
					80					85					90
10	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln
					95					100					105
	Ser	Leu	Leu	Gly	Thr	Gln	Leu	Pro	Pro	Gln	Gly	Arg	Thr	Thr	Ala
					110					115					120
15	His	Lys	Asp	Pro	Asn	Ala	Ile	Phe	Leu	Ser	Phe	Gln	His	Leu	Leu
					125					130					135
	Arg	Gly	Lys	Val	Arg	Phe	Leu	Met	Leu	Val	Gly	Gly	Ser	Thr	Leu
20					140					145					150
	Cys	Val	Arg	Arg	Ala	Pro	Pro	Thr	Thr	Ala	Val	Pro	Ser	Arg	Thr
					155					160					165
25	Ser	Leu	Val	Leu	Thr	Leu	Asn	Gln	Leu	Pro	Asn	Arg	Thr	Ser	Gly
					170					175					180
	Leu	Leu	Glu	Thr	Asn	Phe	Thr	Ala	Ser	Ala	Arg	Thr	Thr	Gly	Ser
					185					190					195
30	Gly	Leu	Leu	Lys	Trp	Gln	Gln	Gly	Phe	Arg	Ala	Lys	Ile	Pro	Gly
					200					205					210
	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Ser	Leu	Asp	Gln	Ile	Pro	Gly	Tyr
35					215					220					225
	Leu	Asn	Arg	Ile	His	Glu	Leu	Leu	Asn	Gly	Thr	Arg	Gly	Leu	Phe
					230					235					240
40	Pro	Gly	Pro	Ser	Arg	Arg	Thr	Leu	Gly	Ala	Pro	Asp	Ile	Ser	Ser
					245					250					255
	Gly	Thr	Ser	Asp	Thr	Gly	Ser	Leu	Pro	Pro	Asn	Leu	Gln	Pro	Gly
					260					265					270
45	Tyr	Ser	Pro	Ser	Pro	Thr	His	Pro	Pro	Thr	Gly	Gln	Tyr	Thr	Leu
					275					280					285
	Phe	Pro	Leu	Pro	Pro	Thr	Leu	Pro	Thr	Pro	Val	Val	Gln	Leu	His
50					290					295					300

Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser
305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln
320 325 330

Glu Gly
332

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
1 5 10 15

Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
20 25 30

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
35 40 45

Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
50 55 60

Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
65 70 75

Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
80 85 90

Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
95 100 105

Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
110 115 120

Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
125 130 135

Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
140 145 150

Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
155 160 165

Arg
166

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG 50
AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC 100
ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG 150
ATTTGCTCCT GCGGGCCATG CTTCTTGCTG TGGCAAGACT AACTCTGTCC 200
AGCCCCGTAG CTCCTGCCTG TGACCCCAAG CTCCTAAATA AACTGCTGCG 250
TGACTCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC 300
CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA 350
TGGAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT 400
GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT 450
CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC 500
TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA 550
CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACCTG CTTGCGGGCA 600
AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG 650

ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT 700

5 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG 750

TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC 800

10 AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT 850

CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAAGTC 900

15 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC 950

20 TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG 1000

ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC 1050

25 CTTACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC 1100

CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC 1150

30 AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG 1200

B'
 COT.
 GGCCTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC 1250

AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTCT GCTTTCACCT 1300

40 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG 1350

GAGCTATTTT TTTTAACT ATCAGCAATA TTCATCAGAG CAGCTAGCGA 1400

45 TCTTTGGTCT ATTTTCGGTA TAAATTGAA AATCACTAAT TCT 1443

50 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu Ala Val
1 5 10 15
10 Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp Pro
20 25 30
Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
35 40 45
15 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val
50 55 60
20 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
65 70 75
Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu
80 85 90
25 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
95 100 105
Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
110 115 120
30 Leu Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu
125 130 135
Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu
140 145 150
Ser Leu Gln Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu
155 160 165
40 Val Glu Gly Pro Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr
170 175 180
Ala Val Pro Ser Ser Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe
185 190 195
45 Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Ser Val Thr
200 205 210
Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg Leu Gln Gly Phe
215 220 225
50

Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr Ser Arg Ser
230 235 240

5 Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly Pro Val
245 250 255

Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr Leu
260 265 270

10 Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu
275 280 285

Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala
290 295 300

15 Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr
305 310 315

20 Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro
320 325 330

Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met
335 340 345

25 Tyr Pro His Pro Arg Asn Leu Ser Gln Glu Thr
350 355 356

(2) INFORMATION FOR SEQ ID NO:10:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser Pro Val Ala Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15

40 Leu Arg Asp Ser His Leu Leu His Ser Arg Leu Ser Gln Cys Pro
20 25 30

Asp Val Asp Pro Leu Ser Ile Pro Val Leu Leu Pro Ala Val Asp
35 40 45

45 Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu Gln Ser Lys Ala
50 55 60

50 Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu Gly Val Met
65 70 75

	Ala	Ala	Arg	Gly	Gln	Leu	Glu	Pro	Ser	Cys	Leu	Ser	Ser	Leu	Leu	
					80					85					90	
5	Gly	Gln	Leu	Ser	Gly	Gln	Val	Arg	Leu	Leu	Leu	Gly	Ala	Leu	Gln	
					95					100					105	
	Gly	Leu	Leu	Gly	Thr	Gln	Gly	Arg	Thr	Thr	Ala	His	Lys	Asp	Pro	
					110					115					120	
10	Asn	Ala	Leu	Phe	Leu	Ser	Leu	Gln	Gln	Leu	Leu	Arg	Gly	Lys	Val	
					125					130					135	
	Arg	Phe	Leu	Leu	Leu	Val	Glu	Gly	Pro	Thr	Leu	Cys	Val	Arg	Arg	
					140					145					150	
15	Thr	Leu	Pro	Thr	Thr	Ala	Val	Pro	Ser	Ser	Thr	Ser	Gln	Leu	Leu	
					155					160					165	
	Thr	Leu	Asn	Lys	Phe	Pro	Asn	Arg	Thr	Ser	Gly	Leu	Leu	Glu	Thr	
20					170					175					180	
	Asn	Phe	Ser	Val	Thr	Ala	Arg	Thr	Ala	Gly	Pro	Gly	Leu	Leu	Ser	
					185					190					195	
25	Arg	Leu	Gln	Gly	Phe	Arg	Val	Lys	Ile	Thr	Pro	Gly	Gln	Leu	Asn	
					200					205					210	
	Gln	Thr	Ser	Arg	Ser	Pro	Val	Gln	Ile	Ser	Gly	Tyr	Leu	Asn	Arg	
					215					220					225	
30	Thr	His	Gly	Pro	Val	Asn	Gly	Thr	His	Gly	Leu	Phe	Ala	Gly	Thr	
					230					235					240	
	Ser	Leu	Gln	Thr	Leu	Glu	Ala	Ser	Asp	Ile	Ser	Pro	Gly	Ala	Phe	
35					245					250					255	
	Asn	Lys	Gly	Ser	Leu	Ala	Phe	Asn	Leu	Gln	Gly	Gly	Leu	Pro	Pro	
					260					265					270	
40	Ser	Pro	Ser	Leu	Ala	Pro	Asp	Gly	His	Thr	Pro	Phe	Pro	Pro	Ser	
					275					280					285	
	Pro	Ala	Leu	Pro	Thr	Thr	His	Gly	Ser	Pro	Pro	Gln	Leu	His	Pro	
					290					295					300	
45	Leu	Phe	Pro	Asp	Pro	Ser	Thr	Thr	Met	Pro	Asn	Ser	Thr	Ala	Pro	
					305					310					315	
	His	Pro	Val	Thr	Met	Tyr	Pro	His	Pro	Arg	Asn	Leu	Ser	Gln	Glu	
50					320					325					330	

Thr
331

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ser Pro Ala Pro Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Ser Val Leu His Gly Arg Leu
20 25 27

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Leu
1 5 10 15
Leu Arg Asp Asp His Val Leu His Gly Arg
20 25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Pro Ala Pro Pro Ala Xaa Asp Pro Arg Leu Xaa Asn Lys
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Arg Leu Leu Asn Lys Leu Leu Arg
1 5 9

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCGTGAAGG ACGTGGTCGT CACGAAGCAG TTTATTTAGG AGTCG 45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCNGCNCNCNC CNGCNTGYGA 20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

NCCRTGNARN ACRTGRTCRT C 21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGCGCCGC CAGCCTGTGA CCCCCGACTC CTAAATAAAC TGCCTCGTGA 50
TGACCACGTT CAGCACGGC 69

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCGCGGCG GTCGGACACT GGGGGCTGAG GATTATTG AC GGAGCACT 50
ACTGGTGCAA GTCGTGCCG 69

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCAGCACCTC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50
CGACCACGTC CATCACGGC 69

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGTCGTGGAG GCCGTACACT GGGGGCTGAG GATTATTTG ACGAAGCACT 50

GCTGGTGCAG GTAGTGCCG 69

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCAGCACCGC CGGCATGTGA CCCCCGACTC CTAAATAAAC TGCTTCGTGA 50

CGATCATGTC TATCACGGT 69

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGTCGTGGCG GCCGTACACT GGGGGCTGAG GATTATTTG ACGAAGCACT 50

GCTAGTACAG ATAGTGCCA 69

B1
35
Cont

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCTAGCTCTA GAAATTGCTC CTCGTGGTCA TGCTTCT 37

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGTCTGCCG TGAAGGACAT GG 22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu
1 5 10 15

Leu Arg Asp Ser His Val Leu His
20 23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro
1 5 10 15

Val Leu Leu Pro Ala Val Asp Phe
20 23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln
1 5 10 15

Asp Ile Leu Gly Ala Val Thr Leu
20 23

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
1 5 10 15

Cys Leu Ser Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu
1 5 10 15

Gln Ser Leu
18

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys
1 5 10 15

Asp Pro Asn Ala Ile Phe
20 21

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met
1 5 10 15

Leu Val Gly Gly Ser Thr Leu Cys Val Arg
20 25